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APR 2 2 2004 EQUENCE LISTING
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Nagata, Leslie P. Wong, JonathAn P. <110> A STRAIN OF THE WESTERN EQUINE ENCEPHALITIS VIRUS (AS AMENDED) <120> <130> **NEL-001** <140> 10/023,649 <141> 2001-12-21 <150> 60/256,948 2000-12-21 <151> <160> <170> PatentIn version 3.1 <210> 11484 <211> <212> DNA <213> Western equine encephalomyelitis virus - strain 71v-1658 <220> <221> **CDS** (25)..(7428) 5' UTR <1 .. 24 <222> <223> <220> <221> **CDS** (7473)..(11183) <222> <223> encodes nucleocapsid, E3, E2, 6K and E1 proteins <400> accctacaaa ctaatcgatc caat atg gaa aga att cac gtt gac tta gat Met Glu Arg Ile His Val Asp Leu Asp 51 gct gac agc ccg tat gtc aag tcg tta cag cgg acg ttt cca caa ttt Ala Asp Ser Pro Tyr Val Lys Ser Leu Gln Arg Thr Phe Pro Gln Phe 99 gạg atc gạa gca agg cạg gtc act gac aat gac cat gcc aat gcc aga 147 Glu Ile Glu Ala Arg Gln Val Thr Asp Asn Asp His Ala Asn Ala Arg gcg ttt tcg cat gtg gca aca aag ctc att gag agc gaa gtc gac cgg Ala Phe Ser His Val Ala Thr Lys Leu Ile Glu Ser Glu Val Asp Arg 195 50 gac caa gtt atc ttg gac att gga agt gcg ccc gtc aga cat gca cat Asp Gln Val Ile Leu Asp Ile Gly Ser Ala Pro Val Arg His Ala His 60 65 70243 tcc aat cac cgc tat cat tgt atc tgc cct atg ata agc gct gaa gac Ser Asn His Arg Tyr His Cys Ile Cys Pro Met Ile Ser Ala Glu Asp 75 80 85 291 ccg gac aga cta caa cgg tat gca gaa aga ctt aag aaa agt gac att Pro Asp Arg Leu Gln Arg Tyr Ala Glu Arg Leu Lys Lys Ser Asp Ile 90 95 100 105 339 acc gac aag aac ata gcc tct aag gcg gca gac ctg ctg gaa gtc atg 387 Thr Asp Lys Asn Ile Ala Ser Lys Ala Ala Asp Leu Glu Val Met tca aca cca gac gca gag act cca tct ctg tgt atg cac aca gac gcc 435

Ser	Thr	Pro	Asp 125	Ala	Glu	Thr	Pro	Ser 130	Leu	Cys	Met	ніѕ	Thr 135	Asp	Ala	
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gtc Val	cat His 155	gca Ala	ccg Pro	aca Thr	tca Ser	atc Ile 160	tac Tyr	cac His	cag Gln	gcg Ala	ctt Leu 165	aaa Lys	gga Gly	gtt Val	agg Arg	531
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atg Met	gca Ala	ggt Gly	tcc Ser	tac Tyr 190	cct Pro	act Thr	tac Tyr	aac Asn	acg Thr 195	aac Asn	tgg Trp	gct Ala	gac Asp	gag Glu 200	aga Arg	627
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cag Gln	aac Asn	tat Tyr 380	cta Leu	tta Leu	cca Pro	gtg Val	gtc Val 385	gcc Ala	cag Gln	gcg Ala	ttt Phe	tcc Ser 390	agg Arg	tgg Trp	gcg Ala	1203
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										4							

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aaa Lys 970	tat Tyr	ccc Pro	ggg Gly	Asp	ttc Phe 975	acg Thr	gct Ala	tca t Ser L	eu A	ac g sp A 80	ac t sp T	gg c rp G	ag cg In Ar	c gaa g Glu 985	2979
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gat Asp	ttg Leu	gga Gly	ata Ile 1200	Pro	agc Ser	cat His	gtc Val	ggt Gly 1205	aaa Lys	tat Tyr	gac Asp	att Ile	atc Ile 1210	ttt Phe	3657
gtc	aat	gtt	agg	acc	ccg	tac	agg	aac	cat 5	cac	tac	caa	cag	tgc _.	3702

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Val	Asn	٧a٦	Arg 1215	Thr	Pro	Tyr	Arg	Asn 1220	His	His	Tyr	Gln	Gln 1225	Cys		
			gct Ala 1230	Ile				atg					gct		3747	
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ctt Leu	gct Ala	gat Asp	cgc Arg 1260	gca Ala	acc Thr	gag Glu	aat Asn	atc Ile 1265	atc Ile	act Thr	gcg Ala	gtg Val	gca Ala 1270	cgc Arg	3837	
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cat His	cac His	ctg Leu	ttc Phe 1455	act Thr	gct Ala	ttc Phe	gac Asp	act Thr 1460	acg Thr	gat Asp	gcc Ala	gat Asp	gtc Val 1465	acc Thr	4422	
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1470		1475	1480		
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agt Ser	att Ile	cca Pro	agt Ser 1755	Ala	tca Ser	ggc Gly	ttt Phe	gaa Glu 1760	val	aga Arg	aca Thr	cca Pro	tct Ser 176		5322
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			gta Val 1800	Pro				aga Arg 1805	Arg	ccc Pro				cct Pro)	5457
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gat Asp	cgg Arg	gcc Ala	val	cat His 1890	gag Glu	aag Lys	tat Tyr	Tyr	gcc Ala 1895	ccg Pro	cgc Arg	ctc Leu	gat Asp	ctc Leu 1900	5727
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gaa Glu	gga Gly	aat Asn	aga Arg	agc Ser 1920	agg Arg	tat Tyr	caa Gln	Ser	cga Arg 1925	aaa Lys	gta Val	gaa Glu	aat Asn	atg Met 1930	5817
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									tac Tyr 2030		aag Lys				6132
				gag Glu 2040		aga Arg	tca Ser	gcc Ala	gtc Val 2045		tcg Ser				6177
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aac Asn	gtt Val	acc Thr	caa Gln	atg Met 2070	cga Arg	gaa Glu	tta Leu	cct Pro	gtc Val 2075		gat Asp				6267
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gtt Val	acg Thr	caa Gln	tat Tyr	gtg Val 2115	aca Thr	aag Lys	ctg Leu	aaa Lys	ggg Gly 2120		aaa Lys	gca Ala	gca Ala	gca Ala 2125	6402
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ccc Pro	ggc Gly	acg Thr	Lys	cat His 2160	Thr	gag Glu	gag Glu	cgg Arg	cct Pro 2165	Lys	gtg val	cag Gln	gtt Val	att Ile 2170	6537
cag Gln	gct Ala	gca Ala	gat Asp	ccc Pro 2175	ctt Leu	gct Ala	acc Thr	gct Ala	tac Tyr 2180		tgc Cys				6582
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gct Ala	gaa Glu	cat His	ttc Phe	cac His 2220	cac His	ggc Gly	gac Asp	cca Pro	gta Val 2225		gaa Glu				6717
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aca Thr	gga Gly	acg Thr	agg Arg	ttt Phe 2280	aaa Lys	ttt Phe	ggt Gly	gcc Ala	atg Met 2285			tcc Ser			6897
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aag Lys	gcc Ala	gta Val	gaa Glu	tcc Ser 2430	aga Arg	tac Tyr	gag Glu	atc Ile	ata Ile 2435	ctg Leu	gca Ala	ggc Gly	ctg Leu	atc Ile 2440	7347
		tct Ser			acg Thr	tta Leu	gcc Ala	gaa Glu	agc Ser 2450	gtt Val	aag Lys	aac Asn	ttc Phe	aag Lys 2455	7392
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tgad	gtag	jta g	acac	gcaco	tad	ccac	cgg	caga	atg Met	ttt Phe	cca Pro	tac Tyr 2470	Pro	cag Gln	7490
	aac Asn		Pro	cca Pro	gtt Val	tac Tyr	cct Pro 2480	Thr	aat Asn	ccg Pro	atg Met	gct Ala 2485	Tyr	cga Arg	7535
_	cca Pro		cct Pro	cct Pro	agg Arg	cgc Arg			agg Arg 10	Pro				ccg Pro	7580

		2490					2495					2500				
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		aaa Lys 2520	caa Gln	cga Arg	tca Ser	cct Pro	aat Asn 2525	ccg Pro	ccg Pro	cca Pro	ggt Gly	cca Pro 2530		cca Pro		7670
	aag Lys	aag Lys 2535					aag Lys 2540		aaa Lys					aaa Lys		7715
		aag Lys 2550	cag Gln	caa Gln	gcc Ala	aag Lys	agg Arg 2555	acg Thr	aaa Lys	cgc Arg	aag Lys	cct Pro 2560		cca Pro		7760
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		atc Ile 2580	atg Met	ctg Leu	aac Asn	ggc Gly	caa Gln 2585	gtg val	aat Asn	gga Gly	tat Tyr	gcc Ala 2590	tgc Cys			7850
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	aat Asn	gag Glu 2610	caa Gln	tta Leu	gcg Ala	gcc Ala	gtg Val 2615	aaa Lys	ttg Leu				agc Ser	atg Met		7940
		ttg Leu 2625		tac Tyr	ggc Gly	gac Asp	gtt Val 2630	ccc Pro	cag Gln					gac Asp		7985
		cag Gln 2640					aaa Lys 2645	cca Pro	ccg Pro	ggc Gly	ttc Phe	tac Tyr 2650	aac Asn	tgg Trp		8030
cac His	cac His	ggc Gly 2655	gca Ala	gtc Val	cag Gln	tat Tyr	gag Glu 2660	aat Asn	ggg Gly	aga Arg	ttt Phe	acc Thr 2665	gta Val	_		8075
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	-	att Ile 2715	agg Arg	gat Asp	acc Thr	ccc Pro	gaa Glu 2720	ggt Gly	tct Ser	gaa Glu	ccg Pro	tgg Trp 2725	tca Ser	cta Leu		8255
gtt Val	aca Thr	gcg Ala 2730	cta Leu	tgc Cys	gtg Val	ctt Leu	tcg Ser 2735	aat Asn	gtc Val	acg Thr	ttc Phe	cca Pro 2740	tgc Cys			8300
	cca Pro	ccc Pro 2745	gtg Val	tgc Cys	tat Tyr	tca Ser	ctg Leu 2750	acg Thr	cca Pro	gaa Glu	cga Arg	aca Thr 2755	ctc Leu		,	8345

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	cga Arg	acg Thr 3000	aag Lys	atg Met	aac Asn	ggc Gly	tgc Cys 3005	act Thr	aaa Lys	gca Ala	aaa Lys	cag Gln 3010	tgc Cys		9110

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ctt Leu	att Ile	agg Arg 3030	cac His	aca Thr	gac Asp	cac His	tca Ser 3035	gtg Val	caa Gln	ggt Gly	aaa Lys	ttg Leu 3040		att Ile	9200
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ggc a	agc Ser	ata Ile 3615	aca Thr	cta Leu	cat His	ttt Phe	agc ser 3620	aca Thr	tcg Ser	agc Ser	cca Pro	caa Gln 3625	gca Ala		10955
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aaaaa	acac	ta ta	acaca	acttt	ata	aatt	ctt 1	tata	attt	t to	ctttt	gttt	ttat	tttgtt	11473
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<210> <211> <212> <213> 2 1852 PRT

Western equine encephalomyelitis virus - strain 71v-1658

<400> 2

Met Glu Arg Ile His Val Asp Leu Asp Ala Asp Ser Pro Tyr Val Lys $1 \hspace{1cm} 15$

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65 70 75 80 Ile Cys Pro Met Ile Ser Ala Glu Asp Pro Asp Arg Leu Gln Arg Tyr 85 90 95 Ala Glu Arg Leu Lys Lys Ser Asp Ile Thr Asp Lys Asn Ile Ala Ser 100 105 110 Lys Ala Ala Asp Leu Leu Glu Val Met Ser Thr Pro Asp Ala Glu Thr 115 120 125 Pro Ser Leu Cys Met His Thr Asp Ala Thr Cys Arg Tyr Phe Gly Ser 130 140 Val Ala Val Tyr Gln Asp Val Tyr Ala Val His Ala Pro Thr Ser Ile 145 150 155 160 Tyr His Gln Ala Leu Lys Gly Val Arg Thr Ile Tyr Trp Ile Gly Phe 165 170 175 Asp Thr Thr Pro Phe Met Tyr Lys Asn Met Ala Gly Ser Tyr Pro Thr 180 185 190 Tyr Asn Thr Asn Trp Ala Asp Glu Arg Val Leu Glu Ala Arg Asn Ile 195 200 205 Gly Leu Gly Asn Ser Asp Leu Gln Glu Ser Arg Leu Gly Lys Leu Ser 210 215 220 Ile Leu Arg Lys Lys Arg Leu Gln Pro Thr Asn Lys Ile Ile Phe Ser 235 240 Val Gly Ser Thr Ile Tyr Thr Glu Asp Arg Ser Leu Leu Arg Ser Trp 245 250 255 His Leu Pro Asn Val Phe His Leu Lys Gly Lys Ser Asn Phe Thr Gly 260 265 270 Arg Cys Gly Thr Ile Val Ser Cys Glu Gly Tyr Val Ile Lys Lys Ile 275 280 285

Thr Ile Ser Pro Gly Leu Tyr Gly Lys Val Glu Asn Leu Ala Ser Thr 290 295 300 Met His Arg Glu Gly Phe Leu Ser Cys Lys Val Thr Asp Thr Leu Arg 305 310 315 320 Gly Glu Arg Val Ser Phe Ala Val Cys Thr Tyr Val Pro Ala Thr Leu 325 330 335 Cys Asp Gln Met Thr Gly Ile Leu Ala Thr Asp Val Ser Val Asp Asp 340 345 350 Ala Gln Lys Leu Leu Val Gly Leu Asn Gln Arg Ile Val Val Asn Gly 355 360 Arg Thr Gln Arg Asn Thr Asn Thr Met Gln Asn Tyr Leu Leu Pro Val 370 380 Val Ala Gln Ala Phe Ser Arg Trp Ala Arg Glu His Arg Ala Asp Leu 385 390 395 400 Asp Asp Glu Lys Glu Leu Gly Val Arg Glu Arg Thr Leu Thr Met Gly 405 410 415 Cys Cys Trp Ala Phe Lys Thr Gln Lys Ile Thr Ser Ile Tyr Lys Lys 420 425 430Pro Gly Thr Gln Thr Ile Lys Lys Val Pro Ala Val Phe Asp Ser Phe 435 440 445 Val Ile Pro Arg Leu Thr Ser His Gly Leu Asp Met Gly Phe Arg Arg 450 460 Arg Leu Lys Leu Leu Glu Pro Thr Val Lys Pro Ala Pro Ala Ile 465 470 475 480 Thr Met Ala Asp Val Glu His Leu Arg Gly Leu Gln Gln Glu Ala Glu 485 490 495 Glu Val Ala Ala Glu Glu Ile Arg Glu Ala Leu Pro Pro Leu Leu 500 505 510 Pro Glu Ile Glu Lys Glu Thr Val Glu Ala Glu Val Asp Leu Ile Met 515 520 Gln Glu Ala Gly Ala Gly Ser Val Glu Thr Pro Arg Gly His Ile Arg 530 540 Val Thr Ser Tyr Pro Gly Glu Glu Lys Ile Gly Ser Tyr Ala Ile Leu 545 550 555 560 Ser Pro Gln Ala Val Leu Asn Ser Glu Lys Leu Ala Cys Ile His Pro 17

Leu Ala Glu Gln Val Leu Val Met Thr His Lys Gly Arg Ala Gly Arg 580 585 590 Tyr Lys Val Glu Pro Tyr His Gly Lys Val Ile Val Pro Glu Gly Thr 595 600 605 Ala Val Pro Val Gln Asp Phe Gln Ala Leu Ser Glu Ser Ala Thr Ile 610 620 Val Phe Asn Glu Arg Glu Phe Val Asn Arg Tyr Leu His His Ile Ala 625 630 635 640 Ile Asn Gly Gly Ala Leu Asn Thr Asp Glu Glu Tyr Tyr Lys Thr Val 645 650 655 Lys Thr Gln Asp Thr Asp Ser Glu Tyr Val Phe Asp Ile Asp Ala Arg 660 665 670 Lys Cys Val Lys Arg Glu Asp Ala Gly Pro Leu Cys Leu Thr Gly Asp 675 680 685 Leu Val Asp Pro Pro Phe His Glu Phe Ala Tyr Glu Ser Leu Lys Thr 690 700 Arg Pro Ala Ala Pro His Lys Val Pro Thr Ile Gly Val Tyr Gly Val 705 710 715 720 Pro Gly Ser Gly Lys Ser Gly Ile Ile Lys Ser Ala Val Thr Lys Lys 725 730 735 Asp Leu Val Val Ser Ala Lys Lys Glu Asn Cys Ala Glu Ile Ile Arg 740 745 750 Asp Val Arg Arg Met Arg Met Asp Val Ala Ala Arg Thr Val Asp 755 760 765 Ser Val Leu Leu Asn Gly Val Lys His Pro Val Asn Thr Leu Tyr Ile 770 780 Asp Glu Ala Phe Ala Cys His Ala Gly Thr Leu Leu Ala Leu Ile Ala 785 790 795 800 Ile Val Lys Pro Lys Lys Val Val Leu Cys Gly Asp Pro Lys Gln Cys 805 810 815Gly Phe Phe Asn Met Met Cys Leu Lys Val His Phe Asn His Asp Ile 820 825 830 Cys Thr Glu Val Tyr His Lys Ser Ile Ser Arg Arg Cys Thr Gln Thr 835 840 845

Val Thr Ala Ile Val Ser Thr Leu Phe Tyr Asp Lys Arg Met Lys Thr 850 860

Val Asn Pro Cys Ala Asp Lys Ile Ile Ile Asp Thr Thr Gly Thr Thr 865 870 875 880

Lys Pro His Lys Asp Asp Leu Ile Leu Thr Cys Phe Arg Gly Trp Val 885 890 895

Lys Gln Leu Gln Ile Asp Tyr Lys Asn His Glu Ile Met Thr Ala Ala 900 905 910

Ala Ser Gln Gly Leu Thr Arg Lys Gly Val Tyr Ala Val Arg Tyr Lys 915 920 925

Val Asn Glu Asn Pro Leu Tyr Ser Gln Thr Ser Glu His Val Asn Val 930 935 940

Leu Leu Thr Arg Thr Glu Lys Arg Ile Val Trp Lys Thr Leu Ala Gly 945 950 955 960

Asp Pro Trp Ile Lys Thr Leu Thr Ala Lys Tyr Pro Gly Asp Phe Thr 965 970 975

Ala Ser Leu Asp Asp Trp Gln Arg Glu His Asp Ala Ile Met Ala Arg 980 985 990

Val Leu Asp Lys Pro Gln Thr Ala Asp Val Phe Gln Asn Lys Val Asn 995 1000 1005

Val Cys Trp Ala Lys Ala Leu Glu Pro Val Leu Ala Thr Ala Asn 1010 1015 1020

Ile Val Leu Thr Arg Gln Gln Trp Glu Thr Leu His Pro Phe Lys 1025 1030 1035

His Asp Arg Ala Tyr Ser Pro Glu Met Ala Leu Asn Phe Phe Cys 1040 1050

Thr Arg Phe Phe Gly Val Asp Leu Asp Ser Gly Leu Phe Ser Ala 1055 1060 1065

Pro Thr Val Ala Leu Thr Tyr Arg Asp Gln His Trp Asp Asn Ser 1070 1080

Pro Gly Lys Asn Met Tyr Gly Leu Asn Arg Glu Val Ala Lys Glu 1085 1090 1095

Leu Ser Arg Arg Tyr Pro Cys Ile Thr Lys Ala Val Asp Thr Gly 1100 1110

Arg Val Ala Asp Ile Arg Asn Asn Thr Ile Lys Asp Tyr Ser Pro 1115 1120 1125 Thr Ile Asn Val Val Pro Leu Asn Arg Arg Leu Pro His Ser Leu 1130 1140 Ile Val Asp His Lys Gly Gln Gly Thr Thr Asp His Ser Gly Phe 1145 1150 Lys Met Lys Gly Lys Ser Val Leu Val Ile Gly Asp Pro 1165 Ile Ser Ile Pro Gly Lys Lys Val Glu Ser Met Gly Pro Leu Pro 1175 1180 1185 Thr Asn Thr Ile Arg Cys Asp Leu Asp Leu Gly Ile Pro Ser His 1190 1200 Val Gly Lys Tyr Asp Ile Ile Phe Val Asn Val Arg Thr Pro Tyr 1205 1215 Arg Asn His His Tyr Gln Gln Cys Glu Asp His Ala Ile His His 1220 1230 Ser Met Leu Thr Cys Lys Ala Val His His Leu Asn Thr Gly Gly Thr Cys Val Ala Ile Gly Tyr Gly Leu Ala Asp Arg Ala Thr Glu 1250 1260 Asn Ile Ile Thr Ala Val Ala Arg Ser Phe Arg Phe Thr Arg Val 1265 1270 1275 Cys Gln Pro Lys Asn Thr Ala Glu Asn Thr Glu Val Leu Phe Val 1280 1285 1290 Phe Phe Gly Lys Asp Asn Gly Asn His Thr His Asp Gln Asp Arg 1295 1300 1305 Leu Gly Val Val Leu Asp Asn Ile Tyr Gln Gly Ser Thr Arg Tyr 1310 1320 Glu Ala Gly Arg Ala Pro Ala Tyr Arg Val Ile Arg Gly Asp Ile 1325 1330 1335 Ser Lys Ser Ala Asp Gln Ala Ile Val Asn Ala Ala Asn Ser Lys 1340 1350 Gly Gln Pro Gly Ser Gly Val Cys Gly Ala Leu Tyr Arg Lys Trp 1355 1360 1365

Pro Ala Ala Phe Asp Arg Gln Pro Ile Ala Val Gly Thr Ala Arg 1370 1380 Leu Val Lys His Glu Pro Leu Ile Ile His Ala Val Gly Pro Asn Phe Ser Lys Met Pro Glu Pro Glu Gly Asp Leu Lys Leu Ala Ala 1400 1405 1410 Ala Tyr Met Ser Ile Ala Ser Ile Val Asn Ala Glu Arg Ile Thr 1415 1420 1425 Lys Ile Ser Val Pro Leu Leu Ser Thr Gly Ile Tyr Ser Gly Gly 1430 1440 Lys Asp_ Arg Val Met Gln Ser_ Leu His His Leu Phe Thr Ala Phe Asp Thr Thr Asp Ala Asp Val Thr Ile Tyr Cys Leu Asp Lys Gln Trp Glu Thr Arg Ile Ile Glu Ala Ile His Arg Lys Glu Ser Val 1475 1480 1485 1480 Glu Ile Leu Asp Asp Asp Lys Pro Val Asp Ile Asp Leu Val Arg 1490 1495 1500 Val His Pro Asn Ser Ser Leu Ala Gly Arg Pro Gly Tyr Ser Val 1505 1510 1515 Asn Glu Gly Lys Leu Tyr Ser Tyr Leu Glu Gly Thr Arg Phe His 1520 1530 Gln Thr Ala Lys Asp Ile Ala Glu Ile His Ala Met Trp Pro Asn Lys Ser Glu Ala Asn Glu Gln Ile Cys Leu Tyr Ile Leu Gly Glu 1550 Ser Met Ser Ser Ile Arg Ser Lys Cys Pro Val Glu Glu Ser Glu 1565 1570 1575 Ala Ser Ala Pro Pro His Thr Leu Pro Cys Leu Cys Asn Tyr Ala 1580 1585 1590 Met Thr Ala Glu Arg Val Tyr Arg Leu Arg Ser Ala Lys Lys Glu Gln Phe Ala Val Cys Ser Ser Phe Leu Leu Pro Lys Tyr Arg Ile 1610 1620 Thr Gly Val Gln Lys Leu Gln Cys Ser Lys Pro Val Leu Phe Ser

Gly Val Val Pro Pro Ala Val His Pro Arg Lys Tyr Ala Glu Ile 1640 1650

Ile Leu Glu Thr Pro Pro Pro Pro Ala Thr Thr Val Ile Cys 1655 1660 1665

Glu Pro Thr Val Pro Glu Arg Ile Pro Ser Pro Val Ile Ser Arg 1670 1680

Ala Pro Ser Ala Glu Ser Leu Leu Ser Leu Gly Gly Val Ser Phe 1685 1690 1695

Ser Ser Ser Ala Thr Arg Ser Ser Thr Ala Trp Ser Asp Tyr Asp 1700 1705

Arg Arg Phe Val Val Thr Ala Asp Val His Gln Ala Asn Thr Ser 1715 1720 1725

Thr Trp Ser Ile Pro Ser Ala Pro Gly Leu Asp Val Gln Leu Pro 1730 1740

Ser Asp Val Thr Asp Ser His Trp Ser Ile Pro Ser Ala Ser Gly 1745 1750 1755

Phe Glu Val Arg Thr Pro Ser Val Gln Asp Leu Thr Ala Glu Cys 1760 1765 1770

Ala Lys Pro Arg Gly Leu Ala Glu Ile Met Gln Asp Phe Asn Thr 1785

Ala Pro Phe Gln Phe Leu Ser Asp Tyr Arg Pro Val Pro Ala Pro 1790 1800

Arg Arg Arg Pro Ile Pro Ser Pro Arg Ser Thr Ala Ser Ala Pro 1805 1810 1815

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Val Ala Arg Ala Ile Ser Glu Ala Glu Leu Asp Glu Tyr Ile Arg 1835 1840 1845

Gln His Ser Asn 1850

<210>

614

<211> <212>

Western equine encephalomyelitis virus - strain 71v-1658

<400>

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Ala Leu Phe Ala Asn Thr His Asn Leu Lys Pro Leu Gln Glu Ile Pro 275 280 285 Met Åsp Gln Phe Val Met Asp Leu Lys Arg Asp Val Lys Val Thr Pro 290 295 300 Gly Thr Lys His Thr Glu Glu Arg Pro Lys Val Gln Val Ile Gln Ala 305 310 315 320 Ala Asp Pro Leu Ala Thr Ala Tyr Leu Cys Gly Ile His Arg Glu Leu 325 330 335 Val Arg Arg Leu Asn Ala Val Leu Leu Pro Asn Ile His Thr Leu Phe 340 345 350 Asp Met Ser Ala Glu Asp Phe Asp Ala Ile Ile Ala Glu His Phe His 355 360 365 His Gly Asp Pro Val Leu Glu Thr Asp Ile Ala Ser Phe Asp Lys Ser 370 380 Glu Asp Asp Ala Ile Ala Ile Ser Ala Leu Met Ile Leu Glu Asp Leu 385 390 395 400 Gly Val Asp Gln Pro Leu Leu Asp Leu Ile Glu Ala Ala Phe Gly Asn 405 410 415 Ile Thr Ser Val His Leu Pro Thr Gly Thr Arg Phe Lys Phe Gly Ala 420 425 430 Met Met Lys Ser Gly Met Phe Leu Thr Leu Phe Val Asn Thr Leu Val 435 440 445 Asn Ile Met Ile Ala Ser Arg Val Leu Arg Glu Arg Leu Thr Thr Ser 450 460 Ala Cys Ala Ala Ser Ile Gly Asp Asp Asn Ile Val His Gly Val Val 465 470 475 480 Ser Asp Thr Leu Met Ala Glu Arg Cys Ala Thr Trp Leu Asn Met Glu 485 490 495 Val Lys Ile Ile Asp Ala Val Ile Gly Ile Lys Ala Pro Tyr Phe Cys 500 510 Gly Gly Phe Ile Leu Val Asp Gln Ile Thr Gly Thr Ala Cys Arg Val 515 520 525 Ala Asp Pro Leu Lys Arg Leu Phe Lys Leu Gly Lys Pro Leu Pro Val 530 540 Asp Asp Thr Gln Asp Cys Asp Arg Arg Arg Ala Leu His Asp Glu Ala 24

Met Arg Trp Asn Arg Ile Gly Ile Thr Asp Glu Leu Val Lys Ala Val 565 570 575

555

Glu Ser Arg Tyr Glu Ile Ile Leu Ala Gly Leu Ile Ile Thr Ser Leu 580 585 590

Ser Thr Leu Ala Glu Ser Val Lys Asn Phe Lys Ser Ile Arg Gly Ser 595 600

Pro Ile Thr Leu Tyr Gly 610

<210>

1236

PRT

Western equine encephalomyelitis virus - strain 71v-1658

<400>

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Pro Met Ala Tyr Arg Asp Pro Asn Pro Pro Arg Arg Arg Trp Arg Pro
20 25 30

Phe Arg Pro Pro Leu Ala Ala Gln Ile Glu Asp Leu Arg Arg Ser Ile 35 40 45

Val Asn Leu Thr Phe Lys Gln Arg Ser Pro Asn Pro Pro Pro Gly Pro 50 60

Pro Pro Lys Lys Lys Ser Ala Pro Lys Pro Lys Pro Thr Gln Pro 65 70 75 80

Lys Lys Lys Gln Gln Ala Lys Arg Thr Lys Arg Lys Pro Lys Pro 85 90 95

Gly Lys Arg Gln Arg Met Cys Met Lys Leu Glu Ser Asp Lys Thr Phe 100 105 110

Pro Ile Met Leu Asn Gly Gln Val Asn Gly Tyr Ala Cys Val Val Gly 115 120 125

Gly Arg Leu Met Lys Pro Leu His Val Glu Gly Lys Ile Asp Asn Glu 130 140

Gln Leu Ala Ala Val Lys Leu Lys Lys Ala Ser Met Tyr Asp Leu Glu 145 150 155 160

Tyr Gly Asp Val Pro Gln Asn Met Lys Ser Asp Thr Leu Gln Tyr Thr 165 170 175

Ser Asp Lys Pro Pro Gly Phe Tyr Asn Trp His His Gly Ala Val Gln 180 185 190 Tyr Glu Asn Gly Arg Phe Thr Val Pro Arg Gly Val Gly Gly Lys Gly 195 200 205 Asp Ser Gly Arg Pro Ile Leu Asp Asn Arg Gly Arg Val Val Ala Ile 210 215 220 Val Leu Gly Gly Ala Asn Glu Gly Thr Arg Thr Ala Leu Ser Val Val 225 230 235 240 Thr Trp Asn Gln Lys Gly Val Thr Ile Arg Asp Thr Pro Glu Gly Ser 245 250 255 Glu Pro Trp Ser Leu Val Thr Ala Leu Cys Val Leu Ser Asn Val Thr 260 265 270 Phe Pro Cys Asp Lys Pro Pro Val Cys Tyr Ser Leu Thr Pro Glu Arg 275 280 285 Thr Leu Asp Val Leu Glu Glu Asn Val Asp Asn Pro Asn Tyr Asp Thr 290 295 300 Leu Leu Glu Asn Val Leu Lys Cys Pro Ser Arg Arg Pro Lys Arg Ser 305 310 315 320 Ile Thr Asp Asp Phe Thr Leu Thr Ser Pro Tyr Leu Gly Phe Cys Pro 325 330 335 Tyr Cys Arg His Ser Thr Pro Cys Phe Ser Pro Ile Lys Ile Glu Asn 340 345 350 Val Trp Asp Glu Ser Asp Asp Gly Ser Ile Arg Ile Gln Val Ser Ala 355 360 365 Gln Phe Gly Tyr Asn Gln Ala Gly Thr Ala Asp Val Thr Lys Phe Arg 370 380 Tyr Met Ser Phe Asp His Asp His Asp Ile Lys Glu Asp Ser Met Glu 385 390 395 400 Lys Ile Ala Ile Ser Thr Ser Gly Pro Cys Arg Arg Leu Gly His Lys 405 410 415Gly Tyr Phe Leu Leu Ala Gln Cys Pro Pro Gly Asp Ser Val Thr Val 420 425 430 Ser Ile Thr Ser Gly Ala Ser Glu Asn Ser Cys Thr Val Glu Lys Lys 435 440 445

Ile Arg Arg Lys Phe Val Gly Arg Glu Glu Tyr Leu Phe Pro Pro Val 450 455 460 His Gly Lys Leu Val Lys Cys His Val Tyr Asp His Leu Lys Glu Thr 465 470 475 480 Ser Ala Gly Tyr Ile Thr Met His Arg Pro Gly Pro His Ala Tyr Lys 485 490 495 Ser Tyr Leu Glu Glu Ala Ser Gly Glu Val Tyr Ile Lys Pro Pro Ser 500 505 510 Gly Lys Asn Val Thr Tyr Glu Cys Lys Cys Gly Asp Tyr Ser Thr Gly 515 520 525Ile Val Ser Thr Arg Thr Lys Met Asn Gly Cys Thr Lys Ala Lys Gln 530 540 Cys Ile Ala Tyr Lys Ser Asp Gln Thr Lys Trp Val Phe Asn Ser Pro 545 550 560 Asp Leu Ile Arg His Thr Asp His Ser Val Gln Gly Lys Leu His Ile 565 570 . 575 Pro Phe Arg Leu Thr Pro Thr Val Cys Pro Val Pro Leu Ala His Thr 580 585 590 Pro Thr Val Thr Lys Trp Phe Lys Gly Ile Thr Leu His Leu Thr Ala 595 600 605 Met Arg Pro Thr Leu Leu Thr Thr Arg Lys Leu Gly Leu Arg Ala Asp 610 615 620 Ala Thr Ala Glu Trp Ile Thr Gly Ser Thr Ser Arg Asn Phe Ser Val 625 630 635 640 Gly Arg Glu Gly Leu Glu Tyr Val Trp Gly Asn His Glu Pro Val Arg 645 650 655 Val Trp Ala Gln Glu Ser Ala Pro Gly Asp Pro His Gly Trp Pro His 660 665 670 Glu Ile Ile His Tyr Tyr His Arg His Pro Val Tyr Thr Val Ile 675 680 685 Val Leu Cys Gly Val Ala Leu Ala Ile Leu Val Gly Thr Ala Ser Ser 690 695 700 Ala Ala Cys Ile Ala Lys Ala Arg Arg Asp Cys Leu Thr Pro Tyr Ala 705 710 715 720 Leu Ala Pro Asn Ala Thr Val Pro Thr Ala Leu Ala Val Leu Cys Cys 27

Ile Arg Pro Thr Asn Ala Glu Thr Phe Gly Glu Thr Leu Asn His Leu 740 745 750 Trp Phe Asn Asn Gln Pro Phe Leu Trp Ala Gln Leu Cys Ile Pro Leu 755 760 765 Ala Ala Leu Val Ile Leu Phe Arg Cys Phe Ser Cys Cys Met Pro Phe 770 780 Leu Leu Val Ala Gly Val Cys Leu Gly Lys Val Asp Ala Phe Glu His 785 790 795 800 Ala Thr Thr Val Pro Asn Val Pro Gly Ile Pro Tyr Lys Ala Leu Val 805 810 815 Glu Arg Ala Gly Tyr Ala Pro Leu Asn Leu Glu Ile Thr Val Val Ser 820 825 830 Ser Glu Leu Thr Pro Ser Thr Asn Lys Glu Tyr Val Thr Cys Lys Phe 835 840 845 Thr Val Ile Pro Ser Pro Gln Val Lys Cys Cys Gly Ser Leu Glu 850 860 Cys Lys Ala Ser Ser Lys Ala Asp Tyr Thr Cys Arg Val Phe Gly Gly 865 870 875 880 Val Tyr Pro Phe Met Trp Gly Gly Ala Gln Cys Phe Cys Asp Ser Glu 885 890 895 Asn Thr Gln Leu Ser Glu Ala Tyr Val Glu Phe Ala Pro Asp Cys Thr 900 905 910 Ile Asp His Ala Val Ala Leu Lys Val His Thr Ala Ala Leu Lys Val 915 920 925 Gly Leu Arg Ile Val Tyr Gly Asn Thr Thr Ala His Leu Asp Thr Phe 930 940 Val Asn Gly Val Thr Pro Gly Ser Ser Arg Asp Leu Lys Val Ile Ala 945 950 955 960 Gly Pro Ile Ser Ala Ala Phe Ser Pro Phe Asp His Lys Val Val Ile 965 970 975 Arg Lys Gly Leu Val Tyr Asn Tyr Asp Phe Pro Glu Tyr Gly Ala Met 980 985 990 Lys Pro Gly Ala Phe Gly Asp Ile Gln Ala Ser Ser Leu Asp Ala Thr 995 1000 1005 Asp Ile Val Ala Arg Thr Asp Ile Arg Leu Leu Lys Pro Ser Val 1010 1020Lys Asn Ile His Val Pro Tyr Thr Gln Ala Val Ser Gly Tyr Glu 1025 1030 1035 Met Trp Lys Asn Asn Ser Gly Arg Pro Leu Gln Glu Thr Ala Pro 1040 1045 Phe Gly Cys Lys Ile Glu Val Glu Pro Leu Arg Ala Ser Asn Cys 1055 1060 1065 Ala Tyr Gly His Ile Pro Ile Ser Ile Asp Ile Pro Asp Ala Ala 1070 1080 Phe Val Arg Ser Ser Glu Ser Pro Thr Ile Leu Glu Val Ser Cys Thr Val Ala Asp Cys Ile Tyr Ser Ala Asp Phe Gly Gly Ser Leu 1100 1105 Thr Leu Gln Tyr Lys Ala Asp Arg Glu Gly His Cys Pro Val His 1115 1120 1125 Ser His Ser Thr Thr Ala Val Leu Lys Glu Ala Thr Thr His Val 1130 1140 Thr Ala Val Gly Ser Ile Thr Leu His Phe Ser Thr Ser Ser Pro 1145 1150 1155 Gln Ala Asn Phe Ile Val Ser Leu Cys Gly Lys Lys Ser Thr Cys 1160 1170 Asn Ala Glu Cys Lys Pro Pro Ala Asp His Ile Ile Gly Glu Pro 1175 1180 1185 His Lys Val Asp Gln Glu Phe Gln Ala Ala Val Ser Lys Thr Ser Trp Asn Trp Leu Leu Ala Leu Phe Gly Gly Ala Ser Ser Leu Ile 1205 1210 Val Val Gly Leu Ile Val Leu Val Cys Ser Ser Met Leu Ile Asn 1220 1230 Thr Arg Arg 1235

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Western equine encephalomyelitis virus - strain 71v-1658 <220> <221> CDS (159)..(3869) <222> vector sequence 1-9; 5' Sacl primer 9-20; 3' end of NS4 gene 16-1 14; intragenic region 115-158; polyprotein (C-E3-E2-6K-E1) 159-38 56; pcDW-XH7 nontranslated region 3857-4150 <400> ggccctctag agctcatact ggcaggcctg atcatcacgt ctctgtccac gttagccgaa 60 120 agcgttaaga acttcaagag cataagaggg agcccaatca ccctctacgg ctgacctaaa taggtgacgt agtagacacg cacctaccca ccggcaga atg ttt cca tac cct cag 176 Met Phe Pro Tyr Pro Gln ctg aac ttt cca cca gtt tac cct aca aat ccg atg gct tac cga gat Leu Asn Phe Pro Pro Val Tyr Pro Thr Asn Pro Met Ala Tyr Arg Asp 224 15 cca aac cct cct agg cgc cgc tgg agg ccg ttt cgg ccc ccg ctg gct Pro Asn Pro Pro Arg Arg Arg Trp Arg Pro Phe Arg Pro Pro Leu Ala 25 30 35 272 gct caa atc gaa gat ctt agg agg tcg ata gtc aac ttg act ttc aaa Ala Gln Ile Glu Asp Leu Arg Arg Ser Ile Val Asn Leu Thr Phe Lys 40 45 50320 caa cga tca cct aat ccg ccg cca ggt cca ccg cca aag aag aag Gln Arg Ser Pro Asn Pro Pro Pro Gly Pro Pro Lys Lys Lys Lys 368 agt gct cct aag cca aaa cct act cag cct aaa aag aag aag cag caa 416 Ser Ala Pro Lys Pro Lys Pro Thr Gln Pro Lys Lys Lys Gln Gln gcc aag agg acg aaa cgc aag cct aaa cca ggg aaa cga caa cgt atg Ala Lys Arg Thr Lys Arg Lys Pro Lys Pro Gly Lys Arg Gln Arg Met 90 95 100464 tgt atg aag ttg gag tcg gac aag aca ttt ccg atc atg ctg aac ggc Cys Met Lys Leu Glu Ser Asp Lys Thr Phe Pro Ile Met Leu Asn Gly 105 115 512 560 ctc cac gtt gaa gga aaa att gat aat gag caa tta gcg gcc gtg aaa Leu His Val Glu Gly Lys Ile Asp Asn Glu Gln Leu Ala Ala Val Lys 608 ttg aag aag gct agc atg tac gac ttg gag tac ggc gac gtt ccc cag 656 Leu Lys Lys Ala Ser Met Tyr Asp Leu Glu Tyr Gly Asp Val Pro Gln aac atg aaa tca gac acg ctg cag tac acc agc gac aaa cca ccg ggc Asn Met Lys Ser Asp Thr Leu Gln Tyr Thr Ser Asp Lys Pro Pro Gly 170 175 180 704 ttc tac aac tgg cac cac ggc gca gtc cag tat gag aat ggg aga ttt Phe Tyr Asn Trp His His Gly Ala Val Gln Tyr Glu Asn Gly Arg Phe 752 acc gta ccg aga ggg ggc ggg aaa ggc gac agc gga aga ccg atc Thr Val Pro Arg Gly Val Gly Gly Lys Gly Asp Ser Gly Arg Pro Ile 800

200					203					210					
gac Asp	aac Asn	aga Arg	ggc Gly	aga Arg 220	gtt val	gtg Val	gct Ala	att Ile	gtt Val 225	cta Leu	gga Gly	ggt Gly	gca Ala	aat Asn 230	848
ggc Gly	acg Thr	cgt Arg	acg Thr 235	gcg Ala	ctt Leu	tca Ser	gtg Val	gtc Val 240	act Thr	tgg Trp	aac Asn	cag Gln	aaa Lys 245	ggg Gly	896
acc Thr	att Ile	agg Arg 250	gat Asp	acc Thr	ccc Pro	gaa Glu	ggt Gly 255	tct Ser	gaa Glu	ccg Pro	tgg Trp	tca Ser 260	cta Leu	gtt Val	944
gcg Ala	cta Leu 265	tgc Cys	gtg val	ctt Leu	tcg Ser	aat Asn 270	gtc Val	acg Thr	ttc Phe	cca Pro	tgc Cys 275	gac Asp	aaa Lys	cca Pro	992
gtg Val 280	tgc Cys	tat Tyr	tca Ser	ctg Leu	acg Thr 285	cca Pro	gaa Glu	cga Arg	aca Thr	ctc Leu 290	gac Asp	gtg Val	ctc Leu	gaa Glu	1040
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tgt Cys	cca Pro	tca Ser	cgc Arg 315	cgg Arg	ccc Pro	aaa Lys	cga Arg	agc Ser 320	att Ile	acc Thr	gat Asp	gac Asp	ttc Phe 325	aca Thr	1136
acc Thr	agt Ser	ccc Pro 330	tac Tyr	ctg Leu	ggg Gly	ttc Phe	tgc Cys 335	ccg Pro	tat Tyr	tgc Cys	aga Arg	cac His 340	tca Ser	acg Thr	1184
tgt Cys	ttc Phe 345	agc Ser	cca Pro	ata Ile	aaa Lys	att Ile 350	gag Glu	aac Asn	gtg Val	tgg Trp	gac Asp 355	gaa Glu	tct Ser	gat Asp	1232
gga G1y 360	tcg Ser	att Ile	aga Arg	atc Ile	cag Gln 365	gtc Val	tcg Ser	gca Ala	caa Gln	ttc Phe 370	ggc Gly	tac Tyr	aat Asn	cag Gln	1280
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gag Glu 440	aat Asn	tca Ser	tgc Cys	acc Thr	gtg Val 445	gag Glu	aaa Lys	aag Lys	atc Ile	agg Arg 450	agg Arg	aag Lys	ttt Phe	gtc Val	1520
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cac His	gtt Val	tac Tyr	gat Asp 475	сас His	ttg Leu	aag Lys	gag Glu	Thr 480	Ser	gcc Ala	ggg Gly	tac Tyr	ata Ile 485	acc Thr	1616
	ggly achr ggla gyalo achr ggla ggly achr ggla gyalo achr tys ggly cats ggly tys ggly tys ggly agan cachies ggly tys ggly achr ggly tys ggly achr ggly tys gg	ggty acry acc atte gcg achr acc atte gcg achr acc atte gcg achr acc atte gcg acys acc ycal accys	ggc acg cgt Gly Thr Arg acc att agg 250 gcg cta tgc Cys gtg tgc tat Tyr aac gtc gac Asp tgt cca tca Cys acc agt ccc Asp tgt cca tca Ser acc agt ccc Asp tgt tc agc ser acc agt ccc agc att Gly acc agc att Gly acc acc agc att Gly acc acc acc agc acc gga tcg att Gly acc acc acc gga tcg att Gly acc acc gga tcg att Gly acc gcg Gly Thr Ala cat gac atc His Asp Ile gga ccc cca Gly Pro 410 tgt cct cca Gly Asp cat gac atc gga acc tcys gag acc tcys Ala cat gac atc gcly Cys gag acc tcys acc gdg acc gdg acc gdg acc ccc cca Gly Ccc cca	ggc acg acg acg acg acg acg acg acg acg	ggc acg cgt acg gcg Ala acc att agg gtg tgc cys ryr ser Leu agg gtg ctg cys val ceu acg yal cys yal ser ser cys pro acg att agg att acc atg yal cys ryr ser ceu acg yal cys ryr ser ceu acc agt cys ryr ceu acc agt cys ryr ceu att aga atc acg yal ser ale agg gat yal	ggc acg cgt acg gcg ctt Thr Ile agg gat acc cys val ceu ser acg yal cys val ceu ser acg yal cys val ceu ser acg yal cys val ceu ser acg acg yal cys val ceu ser acg acg yal cys val ceu ser acg acg cys val ceu ser acg acg yal cys ryr ser ceu acg acg yal cys ryr ser ceu acg acg cys cys pro ser acg acg cag ccc acg acg acg acg acg acg	ggc acg Cgt acg gcg ctt tca acc att agg gat acc ccc gaa Thr 11e Arg Asp Thr Pro Glu gcg Cta tgc yal Leu Ser Asp Ala Leu Cys Tyr Ser Leu Thr Pro gtg tgc tat tca Leu Thr Pro gtg tgc tat tca Leu Thr Pro gtg tgc tat tat	ggc acg cgt acg gcg ctt tca gtg fly Thr Arg acg gcg ctt ser val acc att acg gas gat acc ccc gaa ggt acc cys val ceu ser acg gaa acc acc cys val ceu ser acg gaa acc cys tat tca ctg acg acg ccc acg acc gac gac aat ccc acg acg ccc acg acc acc acc ser ccc tac ccg ggg tcc acc acc acc acc acc acc acc acc acc a	ggc acg cgt acg gcg ctt tca gtg gtc acc att agg gat acc ccc gaa ggt tct gcg cta tgc gtg ctt tcg gat gtt gcg cta tgc gtg ctt tcg acg ggt tct gtg tgc tat tca ctg acg acg gat acg gtg tgc tat tca ctg acg cca gaa cga gtg tgc tat tca ctg pro acg gac acg gtg cca tca tgg cca acg acg gtg tca tac tgg pro acg acg gtg tca tac tac tac gag tc tgg gag ttg ttg tac <td>gly acg acg acg acg acg acg acg acg acg acg</td> <td>ggC acg acg acg gcg gcg<td>ggC acg acg gcg ctt tce ser gtg gtg act trp acs acc att acg gat acc ctc ga ggt tct trp acg trp trp acg ggt tct trp trp trp acg ggt tct trp trp</td><td>ggc acg cgt acg gcg cgt ctt tca ggt tct tgg act tgg act tcg gag act tgg tcg gag tcg tgg tcg tgg tcg tgg tcg tgg tcg tgg tcg gag tcg tcg gag tcg tcg<td>ggc acg Cgt acg Cta Leu See Acg Acg Ctc Leu See Acg Acg Acg Cta Leu See Acg Acg Acg Acg Acg Acg Acg Cca Acg Acg<td>ggc arg liver cgt arg graph graph 275 and a lew ser ser val gat 240 arch 17 mm leg arch 275 arch 285 arch 2245 dil lew ser ser val gat 240 arch 17 mm leg arch 2245 arch 2245 arch 245 arch</td></td></td></td>	gly acg	ggC acg acg acg gcg gcg <td>ggC acg acg gcg ctt tce ser gtg gtg act trp acs acc att acg gat acc ctc ga ggt tct trp acg trp trp acg ggt tct trp trp trp acg ggt tct trp trp</td> <td>ggc acg cgt acg gcg cgt ctt tca ggt tct tgg act tgg act tcg gag act tgg tcg gag tcg tgg tcg tgg tcg tgg tcg tgg tcg tgg tcg gag tcg tcg gag tcg tcg<td>ggc acg Cgt acg Cta Leu See Acg Acg Ctc Leu See Acg Acg Acg Cta Leu See Acg Acg Acg Acg Acg Acg Acg Cca Acg Acg<td>ggc arg liver cgt arg graph graph 275 and a lew ser ser val gat 240 arch 17 mm leg arch 275 arch 285 arch 2245 dil lew ser ser val gat 240 arch 17 mm leg arch 2245 arch 2245 arch 245 arch</td></td></td>	ggC acg acg gcg ctt tce ser gtg gtg act trp acs acc att acg gat acc ctc ga ggt tct trp acg trp trp acg ggt tct trp trp trp acg ggt tct trp trp	ggc acg cgt acg gcg cgt ctt tca ggt tct tgg act tgg act tcg gag act tgg tcg gag tcg tgg tcg tgg tcg tgg tcg tgg tcg tgg tcg gag tcg tcg gag tcg tcg <td>ggc acg Cgt acg Cta Leu See Acg Acg Ctc Leu See Acg Acg Acg Cta Leu See Acg Acg Acg Acg Acg Acg Acg Cca Acg Acg<td>ggc arg liver cgt arg graph graph 275 and a lew ser ser val gat 240 arch 17 mm leg arch 275 arch 285 arch 2245 dil lew ser ser val gat 240 arch 17 mm leg arch 2245 arch 2245 arch 245 arch</td></td>	ggc acg Cgt acg Cta Leu See Acg Acg Ctc Leu See Acg Acg Acg Cta Leu See Acg Acg Acg Acg Acg Acg Acg Cca Acg Acg <td>ggc arg liver cgt arg graph graph 275 and a lew ser ser val gat 240 arch 17 mm leg arch 275 arch 285 arch 2245 dil lew ser ser val gat 240 arch 17 mm leg arch 2245 arch 2245 arch 245 arch</td>	ggc arg liver cgt arg graph graph 275 and a lew ser ser val gat 240 arch 17 mm leg arch 275 arch 285 arch 2245 dil lew ser ser val gat 240 arch 17 mm leg arch 2245 arch 2245 arch 245 arch

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act Thr	gac Asp 1015	Ile	cgg Arg	ctg Leu	ctg Leu	aag Lys 102	Pr	t to O Se	t gt er Va	c aa ll Ly	ig aa 's As 10	nc a sn])25	_	ac g His V	_	3242
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	tcg Ser 1165	cta Leu	tgc Cys	ggc Gly	aag Lys	aag Lys 1170	tcc Ser	acc Thr	tgc Cys	aat Asn	gct Ala 1175	gaa Glu	tgt Cys	aaa Lys	3692
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<210> 6 <211> 1236 <212> PRT

Western equine encephalomyelitis virus - strain 71v-1658 <400> Met Phe Pro Tyr Pro Gln Leu Asn Phe Pro Pro Val Tyr Pro Thr Asn $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$ Pro Met Ala Tyr Arg Asp Pro Asn Pro Pro Arg Arg Arg Trp Arg Pro 20 25 30 Phe Arg Pro Pro Leu Ala Ala Gln Ile Glu Asp Leu Arg Arg Ser Ile 35 40 45 Val Asn Leu Thr Phe Lys Gln Arg Ser Pro Asn Pro Pro Gly Pro 50 55 60 Pro Pro Lys Lys Lys Ser Ala Pro Lys Pro Lys Pro Thr Gln Pro 65 70 75 80 Lys Lys Lys Gln Gln Ala Lys Arg Thr Lys Arg Lys Pro Lys Pro 85 90 95 Gly Lys Arg Gln Arg Met Cys Met Lys Leu Glu Ser Asp Lys Thr Phe 100 105 110Pro Ile Met Leu Asn Gly Gln Val Asn Gly Tyr Ala Cys Val Val Gly 115 120 Gly Arg Leu Met Lys Pro Leu His Val Glu Gly Lys Ile Asp Asn Glu 130 140 Gln Leu Ala Ala Val Lys Leu Lys Lys Ala Ser Met Tyr Asp Leu Glu 145 150 155 160 Tyr Gly Asp Val Pro Gln Asn Met Lys Ser Asp Thr Leu Gln Tyr Thr 165 170 175 Ser Asp Lys Pro Pro Gly Phe Tyr Asn Trp His His Gly Ala Val Gln 180 185 190 Tyr Glu Asn Gly Arg Phe Thr Val Pro Arg Gly Val Gly Gly Lys Gly 195 200 205 Asp Ser Gly Arg Pro Ile Leu Asp Asn Arg Gly Arg Val Val Ala Ile 210 215 220 Val Leu Gly Gly Ala Asn Glu Gly Thr Arg Thr Ala Leu Ser Val Val 225 230 235 240 Thr Trp Asn Gln Lys Gly Val Thr Ile Arg Asp Thr Pro Glu Gly Ser 245 250 255 Glu Pro Trp Ser Leu Val Thr Ala Leu Cys Val Leu Ser Asn Val Thr 35

Phe Pro Cys Asp Lys Pro Pro Val Cys Tyr Ser Leu Thr Pro Glu Arg 275 280 285 Thr Leu Asp Val Leu Glu Glu Asn Val Asp Asn Pro Asn Tyr Asp Thr 290 295 300 Leu Leu Glu Asn Val Leu Lys Cys Pro Ser Arg Arg Pro Lys Arg Ser 305 310 315 320 Ile Thr Asp Asp Phe Thr Leu Thr Ser Pro Tyr Leu Gly Phe Cys Pro 325 330 335 Tyr Cys Arg His Ser Thr Pro Cys Phe Ser Pro Ile Lys Ile Glu Asn 340 345 Val Trp Asp Glu Ser Asp Asp Gly Ser Ile Arg Ile Gln Val Ser Ala 355 360 365 Gln Phe Gly Tyr Asn Gln Ala Gly Thr Ala Asp Val Thr Lys Phe Arg 370 375 380 Tyr Met Ser Phe Asp His Asp His Asp Ile Lys Glu Asp Ser Met Glu 385 390 395 400 Lys Ile Ala Ile Ser Thr Ser Gly Pro Cys Arg Arg Leu Gly His Lys 405 410 415 Gly Tyr Phe Leu Leu Ala Gln Cys Pro Pro Gly Asp Ser Val Thr Val 420 425 430 Ser Ile Thr Ser Gly Ala Ser Glu Asn Ser Cys Thr Val Glu Lys Lys 435 440 445 Ile Arg Arg Lys Phe Val Gly Arg Glu Glu Tyr Leu Phe Pro Pro Val 450 460 His Gly Lys Leu Val Lys Cys His Val Tyr Asp His Leu Lys Glu Thr 465 470 475 480 Ser Ala Gly Tyr Ile Thr Met His Arg Pro Gly Pro His Ala Tyr Lys 485 490 495 Ser Tyr Leu Glu Glu Ala Ser Gly Glu Val Tyr Ile Lys Pro Pro Ser 500 510 Gly Lys Asn Val Thr Tyr Glu Cys Lys Cys Gly Asp Tyr Ser Thr Gly 515 525 Ile Val Ser Thr Arg Thr Lys Met Asn Gly Cys Thr Lys Ala Lys Gln 530 540

Cys Ile Ala Tyr Lys Ser Asp Gln Thr Lys Trp Val Phe Asn Ser Pro 545 550 560 Asp Leu Ile Arg His Thr Asp His Ser Val Gln Gly Lys Leu His Ile 565 570 575 Pro Phe Arg Leu Thr Pro Thr Val Cys Pro Val Pro Leu Ala His Thr 580 585 590 Pro Thr Val Thr Lys Trp Phe Lys Gly Ile Thr Leu His Leu Thr Ala 595 600 605 Met Arg Pro Thr Leu Leu Thr Thr Arg Lys Leu Gly Leu Arg Ala Asp 610 615 620 Ala Thr Ala Glu Trp Ile Thr Gly Ser Thr Ser Arg Asn Phe Ser Val 625 630 635 640 Gly Arg Glu Gly Leu Glu Tyr Val Trp Gly Asn His Glu Pro Val Arg 645 650 655 Val Trp Ala Gln Glu Ser Ala Pro Gly Asp Pro His Gly Trp Pro His 660 665 670 Glu Ile Ile His Tyr Tyr His Arg His Pro Val Tyr Thr Val Ile 675 680 685 Val Leu Cys Gly Val Ala Leu Ala Ile Leu Val Gly Thr Ala Ser Ser 690 700 Ala Ala Cys Ile Ala Lys Ala Arg Arg Asp Cys Leu Thr Pro Tyr Ala 705 710 715 720 Leu Ala Pro Asn Ala Thr Val Pro Thr Ala Leu Ala Val Leu Cys Cys 725 730 735 Ile Arg Pro Thr Asn Ala Glu Thr Phe Gly Glu Thr Leu Asn His Leu 740 745 750 Trp Phe Asn Asn Gln Pro Phe Leu Trp Ala Gln Leu Cys Ile Pro Leu 755 760 765 Ala Ala Leu Val Ile Leu Phe Arg Cys Phe Ser Cys Cys Met Pro Phe 770 780 Leu Leu Val Ala Gly Val Cys Leu Gly Lys Val Asp Ala Phe Glu His 785 790 795 800 Ala Thr Thr Val Pro Asn Val Pro Gly Ile Pro Tyr Lys Ala Leu Val 805 810 815

Glu Arg Ala Gly Tyr Ala Pro Leu Asn Leu Glu Ile Thr Val Val Ser 820 825 830 Ser Glu Leu Thr Pro Ser Thr Asn Lys Glu Tyr Val Thr Cys Lys Phe 835 840 His Thr Val Ile Pro Ser Pro Gln Val Lys Cys Gly Ser Leu Glu 850 860 Cys Lys Ala Ser Ser Lys Ala Asp Tyr Thr Cys Arg Val Phe Gly Gly 865 870 875 880 Val Tyr Pro Phe Met Trp Gly Gly Ala Gln Cys Phe Cys Asp Ser Glu 885 890 895 Asn Thr Gln Leu Ser Glu Ala Tyr Val Glu Phe Ala Pro Asp Cys Thr 900 905 910 Ile Asp His Ala Val Ala Leu Lys Val His Thr Ala Ala Leu Lys Val 915 920 925 Gly Leu Arg Ile Val Tyr Gly Asn Thr Thr Ala His Leu Asp Thr Phe 930 940 Val Asn Gly Val Thr Pro Gly Ser Ser Arg Asp Leu Lys Val Ile Ala 945 950 955 960 Gly Pro Ile Ser Ala Ala Phe Ser Pro Phe Asp His Lys Val Val Ile 965 970 975 Arg Lys Gly Leu Val Tyr Asn Tyr Asp Phe Pro Glu Tyr Gly Ala Met
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Phe Val Arg Ser Ser Glu Ser Pro Thr Ile Leu Glu Val Ser Cys 1085 Ala Asp Cys Ile Tyr Ser Ala Asp Phe Gly Gly Ser Leu 1105 1110 Thr Val Thr Leu Gln Tyr Lys Ala Asp Arg Glu Gly His Cys Pro Val His 1115 1120 1125 Ser His Ser Thr Thr Ala Val Leu Lys Glu Ala Thr Thr His Val Thr Ala Val Gly Ser Ile Thr Leu His Phe Ser Thr Ser Ser Pro Gln Ala Asn Phe Ile Val Ser_ Leu Cys Gly Lys Lys Ser Thr Cys Asn Ala Glu Cys Lys Pro Pro Ala Asp His Ile Ile Gly Glu Pro His Lys Val Asp Gln Glu Phe Gln Ala Ala Val Ser Lys Thr Ser 1200 Trp Asn Trp Leu Leu Ala Leu Phe Gly Gly Ala Ser Ser Leu Ile 1210 Val Val Gly Leu Ile Val Leu Val Cys Ser Ser Met Leu Ile Asn 1220 1230 1220 1230 Thr Arg 1235 Arg <210> 4395 <211> <212> <213> Western equine encephalomyelitis virus - STRAIN 71v-1658 <220> <221> CMV promoter <222> (1) . (1260)PVAX vector sequence: 1-196; CMV promoter: 1-115; CMV putative tr anscriptional start site: 125; T7 promoter: 48-167; pvAX multiclo ning region: 168-196; polyprotein (C-E3-E2-6K-E1): 214-4065; pcDW -HX45 nontranslated region: 4066-4348; pcDW-HX45 vector sequence: <223> 4349-4385; pVAX vector sequence: 4386 <400> 7 accaaaatca acgggacttt ccaaaatgtc gtaacaactc cgccccattg acgcaaatgg 60 gcggtaggcg tgtacggtgg gaggtcatat ataagcagag tctctctggc taactagaga 120 acccactgct tactggctta tcgaaattaa tacgactcac tatagggaga cccaagctgg 180 ctagcgttta aacttaagct tggtaccgag ctcatactgg caggcctgat catcacgtct 240 ctgtccacgt tagccgaaag cgttaagaac ttcaagagca taagagggag cccaatcacc 300

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